AMENDMENTS TO THE CLAIMS

1. (Previously Presented) A method for calibrating data scanned from a molecular array, the method comprising:

selecting a molecular array that includes a set of calibrating features, each containing calibrating probes that indiscriminately hybridize, under stringent conditions, to specific target molecules in sample solutions to which the molecular array is intended to be exposed, wherein upon scanning the calibration probes after they have been hybridized with the target molecules, the scanning of the hybridized probes produces signal intensities proportional to the total concentrations of target molecules in the sample solutions, and a set of features containing probes that hybridize to specific target molecules under stringent conditions;

exposing the molecular array to a sample solution;

reading the molecular array to determine signal intensities of the features and calibrating features of the molecular array;

calculating a collective calibration signal intensity from the signal intensities read from the set of calibrating features; and

calculating normalized signal intensities of the features containing probes that hybridize to specific target molecules, based on signal intensities read from features of the molecular array by applying to the signal intensities a normalization function that includes a calculated collective calibration signal.

2. (Previously Presented) The method of claim 1 wherein said probes that hybridize to specific target molecules are oligonucleotides complementary to portions of cDNA products of reverse transcription of eukaryotic mRNA molecules and wherein the calibrating probes are poly(A) oligonucleotides.

3. (Previously Presented) The method of claim 1 wherein said probes that hybridize to specific target molecules are oligonucleotides complementary to portions of cRNA products of reverse transcription of eukaryotic mRNA molecules and wherein the calibrating probes are poly(A) oligonucleotides.

4. (Previously Presented) The method of claim 1 wherein said probes that hybridize to specific target molecules are oligonucleotides complementary to portions of cDNA products of reverse transcription of human mRNA molecules and wherein the calibrating probes are oligonucleotides complementary to cDNA transcripts of Alu repeat sequences common to many human mRNAs.

5. (Previously Presented) The method of claim 1 wherein said probes that hybridize to specific target molecules are oligonucleotides complementary to portions of cDNA products of reverse transcription of mRNA molecules and wherein the calibrating probes are oligonucleotides complementary to a synthetic nucleotide sequence appended to primers for reverse transcription of the mRNA molecules.

6. (Previously Presented) The method of claim 1 wherein said probes that hybridize to specific target molecules are oligonucleotides complementary to portions of cDNA products of reverse transcription of mRNA molecules and wherein the calibrating probes are random-sequence oligonucleotides.

7. (Previously Presented) The method of claim 1,

wherein the calculated collective calibration signal is calculated by calculating a collective calibration signal intensity from the signal intensities read from the calibrating features, and wherein said method further includes calculating a set of collective calibration signal intensities by partitioning the signal intensities generated from the calibrating features into sets of similar calibrating signal intensities and calculating a collective signal intensity for each set, so that the sets of similar calibrating signal intensities each covers a discrete range of signal intensities and so that the discrete ranges of signal intensities span an overall range of signal intensities generated from the probes that hybridize to specific target molecules, and

wherein calculating normalized signal intensities based on signal intensities read from features of the molecular array by applying to the signal intensities a normalization function that includes the calculated collective calibration signal further includes applying to each signal intensity a normalization function that includes the calculated collective calibration signal calculated from the set of calibrating signal intensities within the discrete range of intensities in which the signal intensity generated from the feature of the molecular array is included.

8. (Original) The method of claim 1

wherein calculating a collective calibration signal intensity from the signal intensities read from the set of calibrating features further includes calculating the average calibration signal intensity from the signal intensities read from the set of calibrating features, and

wherein calculating normalized signal intensities based on signal intensities read from features of the molecular array by applying to the signal intensities a normalization function that includes the calculated collective calibration signal further includes dividing each signal intensity by the calculated average calibration signal intensity.

9. (Canceled)

10. (Previously Presented) A method for calibrating data scanned from a molecular array, the method comprising:

selecting a molecular array that includes features and that includes a calibration feature that includes calibrating probes that indiscriminately hybridize to target molecules in sample solutions, the calibration feature thereby producing a signal intensity directly proportional to the total concentrations of target molecules in the sample solutions;

exposing the molecular array to a sample solution;

reading the molecular array to determine signal intensities for the features of the molecular array and for the calibrating feature; and

calculating normalized signal intensities for the features, each normalized signal intensity based on the determined signal intensity for the respective feature and the signal intensity generated by the calibration probe, and each normalized signal intensity being directly mathematically related to a mole fraction of sample molecules that hybridize to the respective feature and inversely mathematically related to a mole fraction of sample molecules that hybridize to the calibration feature.

11. (Previously Presented) The method of claim 10 wherein a plurality of calibration features are included in the molecular array, each calibration feature including calibrating probes that hybridize to target molecules in sample solutions, each said calibration feature thereby producing a signal intensity directly proportional to the total concentration of target molecules in the sample solutions.

12. (Previously Presented) The method of claim 11 wherein a collective calibration signal

intensity is calculated from signal intensities read from said plurality of calibration features, and wherein calculating normalized signal intensities for the features further comprises calculating normalized signal intensities based on the signal intensities read from the features of the molecular array by applying to the signal intensities a normalization function that includes the calculated collective calibration signal.

13. (Canceled)

14. (Canceled)

15. (Previously Presented) The method of claim 1, wherein an average of the signal intensities read from the calibrating features is proportional to the total concentration of target molecules in the sample solution to which the array is exposed.

16. (Canceled)

17. (Canceled)

18. (Currently Amended) The method of claim 1, wherein at least one of the calibrating probes hybridizes ~~hybridize~~ to all of the target molecules in sample solutions.

19. (Canceled)

20. (Currently Amended) The method of claim 10, wherein at least one of the calibrating probes hybridizes ~~hybridize~~ to all of the target molecules in sample solutions.